

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 31, 2005, 18:10:30 ; Search time 28 Seconds  
(without alignments)  
48.108 Million cell updates/sec

Title: US-10-083-768-12

Perfect score: 85

Sequence: 1 CADGPTLREWISFC 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_79:\*\*

1: pir1:\*\*

2: pir2:\*\*

3: pir3:\*\*

4: pir4:\*\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	52.9	108	2 T49731	hypothetical prote
2	44	51.8	974	2 S34189	starch phosphoryla
3	44	51.8	1022	1 S00503	Na+/K+-exchanging
4	44	51.8	1023	2 A24414	Na+/K+-exchanging
5	43	50.6	245	2 T47701	translation initia
6	43	50.6	490	2 T09084	phosphatidylinosit
7	43	50.6	1010	2 B37227	Na+/K+-exchanging
8	43	50.6	1013	1 S00801	Na+/K+-exchanging
9	43	50.6	1013	2 C24639	Na+/K+-exchanging
10	43	50.6	1017	2 A37227	Na+/K+-exchanging
11	43	50.6	1020	2 A34474	Na+/K+-exchanging
12	43	50.6	1020	2 B24639	Na+/K+-exchanging
13	43	50.6	1021	1 PWSHNA	Na+/K+-exchanging
14	43	50.6	1021	1 S04630	Na+/K+-exchanging
15	43	50.6	1021	2 A28199	Na+/K+-exchanging
16	43	50.6	1021	2 B24862	Na+/K+-exchanging
17	43	50.6	1022	2 S49127	Na+/K+-exchanging
18	43	50.6	1023	1 A24639	Na+/K+-exchanging
19	43	50.6	1023	1 S24650	Na+/K+-exchanging
20	43	50.6	1025	2 A60444	Na+/K+-exchanging
21	43	50.6	1027	1 PWCNNM	Na+/K+-exchanging
22	43	50.6	1038	1 S03632	Na+/K+-exchanging
23	42.5	50.0	1004	2 JH0470	Na+/K+-exchanging
24	42	49.4	312	2 F86876	hypothetical prote
25	42	49.4	522	2 D69226	probable membrane
26	42	49.4	522	2 S62941	conserved hypothe
27	42	49.4	725	2 A11544	starch phosphoryla
28	42	49.4	842	2 T12091	hypothetical prote
29	41	48.2	189	2 S07755	hypothetical prote

30	41	48.2	273	2 H70849	hypothetical prote
31	41	48.2	473	2 E84853	hypothetical prote
32	41	48.2	955	2 T10947	starch phosphoryla
33	41	48.2	966	1 PHPOAG	starch phosphoryla
34	41	48.2	971	2 T09210	starch phosphoryla
35	41	48.2	1000	2 S47243	S-layer protein -
36	41	48.2	1616	2 T17884	ribosomal protein
37	40	47.1	98	2 A70301	T-cell receptor be
38	40	47.1	152	2 S21826	interleukin-2 prec
39	40	47.1	169	1 ICMS2	interleukin-2 prec
40	40	47.1	169	2 S37289	hypothetical prote
41	40	47.1	169	2 E95908	pol polyprotein -
42	40	47.1	217	2 S46354	probable hydrolase
43	40	47.1	252	2 B97072	corinoid/iron-sul
44	40	47.1	389	2 B69096	LIS-1 protein - hu
45	40	47.1	409	2 S36113	

ALIGNMENTS

RESULT 1

T49731

hypothetical protein B24B19.30 [imported] - Neurospora crassa

C:Species: Neurospora crassa

C>Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 18-Aug-2000

C:Accession: T49731

R:Schulze, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,

submitted to the Protein Sequence Database, May 2000

A:Reference number: 225022

A:Accession: T49731

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-108 <SCH>

A:Cross-references: EMBL:ALJ56192; GSPDB:GN00116; NCSP:B24B19.30

A:Experimental source: BAC clone B24B19; strain OR74A

C:Genetics:

A:Gene: NCSP:B24B19.30

A:Map position: 6

C:Superfamily: Neurospora crassa hypothetical protein B24B19.30

Query Match 52.9%; Score 45; DB 2; Length 108;  
Best Local Similarity 50.0%; Pred. No. 3.6;  
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CADGPTLREWISFC 14

Db 70 CQCQPILRNWLSWC 83

RESULT 2

S34189

starch phosphorylase (EC 2.4.1.1) L - potato

C:Species: Solanum tuberosum (potato)

C>Date: 03-Mar-1994 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004

C:Accession: S53489; S34189

R:Sonnefeld, U.; Basner, A.; Greve, B.; Steup, M.

Plant Mol. Biol. 27, 567-576, 1995

A:Title: A second L-type isozyme of potato glucan phosphorylase: cloning, antisense inhi

A:Reference number: S53489; MUID:95201249; PMID:7894019

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-974 <S02>

A:Cross-references: UNIPROT:P53535; EMBL:X73684; NID:g313348; PIDN:CAA52036.1; PID:g31333

C:Superfamily: glucan phosphorylase

C:Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein; pyridoxal phosphate

F;820/Binding site: pyridoxal phosphate [Lys] (covalent) #status predicted

Query Match 51.8%; Score 44; DB 2; Length 974;  
Best Local Similarity 58.3%; Pred. No. 43;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 DQPTLRWISFC 14  
: |||||  
Db 619 NGVTPRWLSFC 630

RESULT 3  
S00503  
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - Pacific electric ray  
C:Species: Torpedo californica (Pacific electric ray)  
C:Date: 30-Jun-1993 #sequence revision 30-Jun-1993 #text\_change 09-Jul-2004  
C:Accession: S00503; S28885; S29880  
R:Kawakami, K.; Noguchi, S.; Noda, M.; Takahashi, H.; Ohta, T.; Kawamura, M.; Nojima, H.  
Nature 316, 733-736, 1985  
A:Title: Primary structure of the alpha-subunit of Torpedo californica (Na(+)+K(+))ATPase  
A:Reference number: S00503; MUID:85296307; PMID:2993905  
A:Accession: S00503  
A:Molecule type: mRNA  
A:Residues: 1-1022 <KAW1>  
A:Cross-references: UNIPROT:P05025; EMBL:X02810; NID:g64399; PIDN:CAA26578.1; PID:g64400  
A:Accession: S28885  
A:Molecule type: protein  
A:Residues: 228-240/431-438;535-550/671-690;1011-1022 <KAW2>  
R:Ohta, T.; Nagano, K.; Yoshida, M.  
Proc. Natl. Acad. Sci. U.S.A. 83, 2071-2075, 1986  
A:Title: The active site structure of Na(+)/K(+)-transporting ATPase: location of the 5'  
A:Reference number: S29880; MUID:86177549; PMID:3008150  
A:Accession: S29880  
A:Molecule type: protein  
A:Residues: 386-402/502-512;671-689;887-906 <OHT>  
C:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain  
C:Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transp  
F:96-120/Domain: transmembrane #status predicted <TM1>  
F:130-149/Domain: transmembrane #status predicted <TM2>  
F:150-290/Domain: intracellular #status predicted <TM3>  
F:291-313/Domain: transmembrane #status predicted <TM2>  
F:320-348/Domain: transmembrane #status predicted <TM4>  
F:349-785/Domain: intracellular #status predicted <INT3>  
F:586-782/Domain: ATPase nucleotide-binding domain homology <ATN>  
F:786-809/Domain: transmembrane #status predicted <TM5>  
F:848-873/Domain: transmembrane #status predicted <TM6>  
F:874-951/Domain: intracellular #status predicted <INT4>  
F:952-977/Domain: transmembrane #status predicted <TM7>  
F:978-1022/Domain: extracellular #status predicted <EXT>  
F:3/76/Active site: Asp (aspartylphosphate intermediate) #status predicted  
F:507/Binding site: ATP (Lys) #status predicted  
F:716,720,725/Active site: Asp, Asp, Lys #status predicted

QY 5 PTLREWISFC 14  
: |||||  
Db 84 PTPPEWIKFC 93

RESULT 4  
A24414  
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-1 chain - human  
N:Alternate names: sodium pump; sodium/potassium transporting ATPase alpha-A chain  
C:Species: Homo sapiens (man)  
C:Date: 02-Jun-1988 #sequence revision 02-Jun-1988 #text\_change 09-Jul-2004  
C:Accession: A24414; A27795; A39910; I60116; S09171  
R:Kawakami, K.; Ohta, T.; Nojima, H.; Nagano, K.  
J. Biochem. 100, 389-397, 1986  
A:Title: Primary structure of the alpha-subunit of human Na,K-ATPase deduced from cDNA s  
A:Reference number: A24414; MUID:87057096; PMID:2430951  
A:Accession: A24414  
A:Molecule type: mRNA  
A:Residues: 1-1023 <KAW>  
A:Cross-references: UNIPROT:P05023; EMBL:X04297; NID:g28926; PIDN:CAA27840.1; PID:g28927  
R:Shull, M.M.; Lingrel, J.B.  
Proc. Natl. Acad. Sci. U.S.A. 84, 4039-4043, 1987

A:Title: Multiple genes encode the human Na+,K+-ATPase catalytic subunit.  
A:Reference number: A94158; MUID:87231946; PMID:3035563  
A:Accession: A27795  
A:Molecule type: DNA  
A:Residues: 168-189/213-214,'X',216-244 <SHU>  
R:Chehab, F.F.; Kan, Y.W.; Law, M.L.; Hartz, J.; Kao, F.T.; Blostein, R.  
Proc. Natl. Acad. Sci. U.S.A. 84, 7901-7905, 1987  
A:Title: Human placental Na+,K+-ATPase alpha subunit: cDNA cloning, tissue expression, DN  
A:Reference number: A39910; MUID:88068506; PMID:2891135  
A:Accession: A39910  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 199-942 <CHE>  
A:Cross-references: GB:J03007  
R:Shull, M.M.; Pugh, D.G.; Lingrel, J.B.  
Genomics 6, 451-460, 1990  
A:Title: The human Na, K-ATPase alpha 1 gene: characterization of the 5'-flanking region  
A:Reference number: I60116; MUID:90228961; PMID:1970326  
A:Accession: I60116  
A:Status: translation not shown; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-61 <RES>  
A:Cross-references: GB:M30310; NID:g179206; PIDN:AAAS1801.1; PID:g179208  
C:Genetics:  
A:Gene: GDB:ATP1A1  
A:Map Position: 1p13-lp11  
C:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain  
C:Keywords: ATP; heterodimer; hydrolase; ion transport; osmoregulation; phosphoprotein; i  
F:6-1023/Domain: intracellular #status predicted <INT1>  
F:96-120/Domain: transmembrane #status predicted <TM1>  
F:130-149/Domain: transmembrane #status predicted <TM2>  
F:150-290/Domain: intracellular #status predicted <TM3>  
F:291-313/Domain: transmembrane #status predicted <TM2>  
F:320-348/Domain: transmembrane #status predicted <TM4>  
F:349-786/Domain: intracellular #status predicted <INT3>  
F:587-783/Domain: ATPase nucleotide-binding domain homology <ATN>  
F:787-810/Domain: transmembrane #status predicted <TM5>  
F:849-874/Domain: transmembrane #status predicted <TM6>  
F:895-952/Domain: intracellular #status predicted <INT4>  
F:953-978/Domain: transmembrane #status predicted <TM7>  
F:979-1023/Domain: extracellular #status predicted <EXT>  
F:3/76/Active site: Asp (aspartylphosphate intermediate) #status predicted  
F:508/Binding site: ATP (Lys) #status predicted  
F:717,721,726/Active site: Asp, Asp, Lys #status predicted

Query Match 51.8%; Score 44; DB 2; Length 1023;  
Best Local Similarity 70.0%; Pred. No. 45;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 PTLREWISFC 14  
: |||||  
Db 84 PTPPEWIKFC 93

RESULT 5  
T47701  
translation initiation factor eIF-6-like protein [imported] - Arabidopsis thaliana  
N:Alternate names: protein F116.30  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C:Accession: T47701  
R:Benes, V.; Wurmbach, E.; Drzonek, H.; Ansorge, W.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.  
submitted to the Protein Sequence Database, March 2000  
A:Reference number: 224473  
A:Accession: T47701  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-245 <BEN>  
A:Cross-references: UNIPROT:Q9M060; EMBL:AL161667  
A:Experimental source: cultivar Columbia; BAC clone F1116  
C:Genetics:

A:Map position: 3  
A:Introns: 4/1; 36/2; 65/1; 80/1; 123/3; 160/3  
A:Note: F116.30  
C:Superfamily: conserved hypothetical protein YPR016C

Query Match 50.6%; Score 43; DB 2; Length 245;  
Best Local Similarity 53.8%; Pred. No. 17;  
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ADGPTLRWISFC 14  
| | | | |  
Db 194 AAGMTVNDWTSC 206

RESULT 6  
T09084  
phosphatidylinositol 3-kinase - Chlamydomonas reinhardtii (fragment)  
C:Species: Chlamydomonas reinhardtii  
C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C:Accession: T09084  
R:Molendijk, A.J.; Irvine, R.F.  
Plant Mol. Biol. 37, 53-66, 1998  
A:Title: Inositolide signalling in Chlamydomonas: Characterization of a phosphatidylinositol 3-kinase  
A:Reference number: 216411; MUID:98281574; PMID:9620264  
A:Accession: T09084  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-490 <MOL>  
A:Cross-references: UNIPROT:O04270; EMBL:U97663; PIDN:AC50018.1; PID:g2102408  
A:Experimental source: strain cw-15  
C:Genetics:  
A:Introns: 265/3; 331/3; 370/3; 455/1; 481/3

Query Match 50.6%; Score 43; DB 2; Length 490;  
Best Local Similarity 57.1%; Pred. No. 32;  
Matches 8; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

Qy 3 DGPTLR--EWISFC 14  
| | | | |  
Db 250 DGSTARWDEWLTF 263

RESULT 7  
B37227  
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-3 chain - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 09-Jul-2004  
C:Accession: B37227; I50395  
R:Takeyasu, K.; Lemas, V.; Fambrough, D.M.  
Am. J. Physiol. 259, C619-C630, 1990  
A:Title: Stability of Na(+)-K(+)-ATPase alpha-subunit isoforms in evolution.  
A:Reference number: A37227; MUID:91023019; PMID:2171348  
A:Accession: B37227  
A:Molecule type: mRNA  
A:Residues: 1-1010 <ATN>  
A:Cross-references: UNIPROT:P24798; GB:M59960; NID:g212407; PIDN:AAA48982.1; PID:g212408  
C:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain  
C:Keywords: ATP; glycoprotein; hydrolase; phosphoprotein; potassium transport; sodium transport  
F:574-770/Domain: ATPase nucleotide-binding domain homology <ATN>  
F:202,470/Binding site: carboxylate (Asn) (covalent) #status predicted  
F:363/Active site: Asp (aspartylphosphate intermediate) #status predicted  
F:495/Binding site: ATP (Lys) #status predicted

Query Match 50.6%; Score 43; DB 2; Length 1010;  
Best Local Similarity 60.0%; Pred. No. 64;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PTLREWISFC 14  
| | | | |  
Db 71 PTPPEWKFC 80

RESULT 8

S00801  
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-3 chain - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 09-Jul-2004  
C:Accession: S00801; S04019; A27397; S02275  
R:Ovchinnikov, Y.A.; Monastyrskaya, G.S.; Broude, N.E.; Ushkaryov, Y.A.; Melkov, A.M.; Sverdlov, N.N.; Sverdlov, E.D.  
FEBS Lett. 233, 87-94, 1988  
A:Title: Family of human Na,K-ATPase genes. Structure of the gene for the catalytic subunit  
A:Reference number: S00801; MUID:88255304; PMID:2838329  
A:Accession: S00801  
A:Molecule type: DNA  
A:Residues: 1-1013 <OVC>  
A:Cross-references: UNIPROT:P13637; EMBL:M37456  
R:Sverdlov, E.D.; Monastyrskaya, G.S.; Broude, N.E.; Ushkarev, Y.A.; Melkov, A.M.; Smirnov, N.N.; Ovchinnikov, Y.A.  
Dokl. Biochem. 297, 426-431, 1987  
A:Title: Family of human Na(+),K(+)-ATPase genes. Structure of the gene of isoform alpha-3  
A:Reference number: S04019  
A:Accession: S04019  
A:Molecule type: DNA  
A:Residues: 1, 'EIH', 3-1013 <SVE1>  
A:Cross-references: EMBL:X12910; NID:928963  
A:Note: The authors translated the codon TTC for residue 283 as Ser and TCT for residue 284 as Ser. This paper is a translation of the Russian paper published in Dokl. Akad. Nauk SSSR.  
R:Sverdlov, E.D.; Monastyrskaya, G.S.; Broude, N.E.; Ushkaryov, Y.A.; Allikmets, R.L.; Modyanov, M.B.; Sverdlov, V.E.; Modyanov, N.N.; Ovchinnikov, Y.A.  
FEBS Lett. 217, 275-278, 1987  
A:Title: The family of human Na+,K+-ATPase genes. No less than five genes and/or pseudogenes  
A:Reference number: A27397; MUID:87247232; PMID:3036582  
A:Accession: A27397  
A:Molecule type: mRNA  
A:Residues: 243-434 <SVE2>  
A:Cross-references: GB:M27570  
C:Genetics:  
A:Gene: GDB:ATPLA3  
A:Cross-references: GDB:119713; OMIM:182350  
A:Map position: 19q13.2-19q13.2  
A:Introns: 2/3; 31/3; 51/3; 119/3; 157/3; 202/3; 242/1; 331/3; 398/1; 435/2; 479/3; 544/3  
C:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain  
C:Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transport  
F:86-110/Domain: transmembrane #status predicted <TM1>  
F:120-139/Domain: intracellular #status predicted <INT2>  
F:140-280/Domain: transmembrane #status predicted <TM2>  
F:281-303/Domain: transmembrane #status predicted <TM3>  
F:310-338/Domain: transmembrane #status predicted <TM4>  
F:339-776/Domain: intracellular #status predicted <INT3>  
F:577-773/Domain: ATPase nucleotide-binding domain homology <ATN>  
F:777-800/Domain: transmembrane #status predicted <TM5>  
F:839-864/Domain: transmembrane #status predicted <TM6>  
F:865-942/Domain: intracellular #status predicted <INT4>  
F:943-968/Domain: transmembrane #status predicted <TM7>  
F:969-1013/Domain: extracellular #status predicted <EXT>  
F:366/Active site: Asp (aspartylphosphate intermediate) #status predicted  
F:498/Binding site: ATP (Lys) #status predicted  
F:707,711,716/Active site: Asp, Asp, Lys #status predicted

Query Match 50.6%; Score 43; DB 1; Length 1013;  
Best Local Similarity 60.0%; Pred. No. 64;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PTLREWISFC 14  
| | | | |  
Db 74 PTPPEWKFC 83

RESULT 9  
C24639  
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-3 chain - rat  
N:Alternate names: Na+/K+-transporting ATPase alpha (III) chain  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Jun-1988 #sequence\_revision 23-Apr-1993 #text\_change 09-Jul-2004  
C:Accession: C24639; S00514; B27180; A60470

R;Shull, G.E.; Greeb, J.; Lingrel, J.B.  
Biochemistry 25, 8125-8132, 1986  
A;Title: Molecular cloning of three distinct forms of the Na<sup>+</sup>, K<sup>+</sup>-ATPase alpha-subunit from  
A;Reference numbers: A90512; MUID:87128908; PMID:3028470  
A;Accession: C24639  
A;Molecule type: mRNA  
A;Residues: 1-1013 <SHU>  
A;Cross-references: UNIPROT:P06587; EMBL:M14513; NID:G203030; PIDN:AAA40777.1; PID:G203030  
A;Note: in the authors' translation 405-Ser is shown after residue 409 and, consequently  
R;Hara, Y.; Urayama, O.; Kawakami, K.; Nojima, H.; Nagamune, H.; Kojima, T.; Ohka, T.; N  
J. Biochem. 102, 43-58, 1987  
A;Title: Primary structures of two types of alpha-subunit of rat brain Na<sup>+</sup>, K<sup>+</sup>-ATPase  
A;Reference number: S00460; MUID:88032933; PMID:2822682  
A;Accession: S00514  
A;Molecule type: mRNA  
A;Residues: 1-907, 'C', 909-1013 <HAR>  
A;Cross-references: EMBL:X05883; NID:G55769; PIDN:CAA29307.1; PID:G55770  
R;Herrera, V.L.M.; Emanuel, J.R.; Ruiz-Opazo, N.; Levenson, R.; Nadal-Ginard, B.  
J. Cell Biol. 105, 1855-1865, 1987  
A;Title: Three differentially expressed Na<sup>+</sup>, K<sup>+</sup>-ATPase alpha subunit isoforms: structural a  
A;Reference number: A92749; MUID:88033255; PMID:2822726  
A;Accession: B27180  
A;Molecule type: mRNA  
A;Residues: 1, 'NL', 4-103, 'R', 105-113, 'E', 115-127, 'G', 129-148, 'Q', 150-151, 'T', 153-165, 'D'  
A;Cross-references: EMBL:M28648; NID:G205633; PIDN:AAA41672.1; PID:G205634  
A;Note: the authors translated the codon CAG for residue 149 as Glu, GGC for residue 194  
R;Hsu, Y.M.; Guidotti, G.  
Biochemistry 28, 569-573, 1989  
A;Title: Rat brain has the alpha3 form of the (Na<sup>+</sup>, K<sup>+</sup>)ATPase.  
A;Reference number: A60470; MUID:89229049; PMID:2540801  
A;Accession: A60470  
A;Molecule type: protein  
A;Residues: 117-132:586-595, 'X', 597-601 <HSU>  
A;Comment: The alpha-3 form appears to be highly ouabain-inhibitable, as is alpha-2 but  
C;Genetics:  
A;Gene: NKAA3  
C;Superfamily: Na<sup>+</sup>/K<sup>+</sup>-transporting ATPase alpha chain; ATPase nucleotide-binding domain  
C;Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transp  
F;86-110/Domain: transmembrane #status predicted <TM1>  
F;120-139/Domain: transmembrane #status predicted <TM2>  
F;140-280/Domain: intracellular #status predicted <INT2>  
F;281-303/Domain: transmembrane #status predicted <TM3>  
F;310-338/Domain: transmembrane #status predicted <TM4>  
F;339-776/Domain: intracellular #status predicted <INT3>  
F;577-773/Domain: ATPase nucleotide-binding domain homology <ATN>  
F;777-800/Domain: transmembrane #status predicted <TM5>  
F;839-864/Domain: transmembrane #status predicted <TM6>  
F;865-942/Domain: intracellular #status predicted <INT4>  
F;943-968/Domain: transmembrane #status predicted <TM7>  
F;969-1013/Domain: transmembrane #status predicted <EXT>  
F;366/Active site: Asp (aspartylphosphate intermediate) #status predicted  
F;498/Binding site: ATP (lys) #status predicted  
F;707,711,716/Active site: Asp, Asp, Lys #status predicted

Query Match 50.6%; Score 43; DB 2; Length 1013;  
Best Local Similarity 60.0%; Pred. No. 64;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 PTLREWISFC 14  
DB 74 PTPENWVFC 83

RESULT 10  
A37227  
Na<sup>+</sup>/K<sup>+</sup>-exchanging ATPase (EC 3.6.3.9) alpha-2 chain - chicken  
C;Species: Gallus gallus (chicken)  
C;Date: 16-Sep-1992 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C;Accession: I50394; A37227  
R;Takeyasu, K.; Lemas, M.; Fambrough, D.M.  
Am. J. Physiol. 259, 619-630, 1991  
A;Title: Stability of the Na<sup>+</sup>, K<sup>+</sup>-ATPase alpha-subunit isoforms in evolution.  
A;Reference number: I50394

A;Accession: I50394  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-1017 <TAK>  
A;Cross-references: UNIPROT:P24797; GB:M59959; NID:G212405; PIDN:AAA48981.1; PID:G212406  
R;Takeyasu, K.; Lemas, V.; Fambrough, D.M.  
Am. J. Physiol. 259, C619-C630, 1990  
A;Title: Stability of Na<sup>+</sup>, K<sup>+</sup>-ATPase alpha-subunit isoforms in evolution.  
A;Reference number: A37227; MUID:91023019; PMID:2171348  
A;Accession: A37227  
A;Molecule type: mRNA  
A;Residues: 3-1017 <TA2>  
C;Superfamily: Na<sup>+</sup>/K<sup>+</sup>-transporting ATPase alpha chain; ATPase nucleotide-binding domain 1.  
C;Keywords: ATP; glycoprotein; hydrolase; ion transport; phosphoprotein  
F;581-777/Domain: ATPase nucleotide-binding domain homology <ATN>  
F;210,478/Binding site: carboxylate (Asn) (covalent) #status predicted  
F;371/Active site: Asp (aspartylphosphate intermediate) #status predicted

Query Match 50.6%; Score 43; DB 2; Length 1017;  
Best Local Similarity 60.0%; Pred. No. 64;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 PTLREWISFC 14  
DB 79 PTPENWVFC 88

RESULT 11  
A34474  
Na<sup>+</sup>/K<sup>+</sup>-exchanging ATPase (EC 3.6.3.9) alpha-2 chain - human  
N;Alternate names: Na<sup>+</sup>/K<sup>+</sup>-exchanging ATPase alpha chain-4; sodium/potassium transporting  
C;Species: Homo sapiens (man)  
C;Date: 15-Jun-1990 #sequence\_revision 15-Jun-1990 #text\_change 09-Jul-2004  
C;Accession: A34474; B27795; D27397  
R;Shull, M.M.; Pugh, D.G.; Lingrel, J.B.  
J. Biol. Chem. 264, 17532-17543, 1989  
A;Title: Characterization of the human Na<sup>+</sup>, K<sup>+</sup>-ATPase alpha2 gene and identification of int  
A;Reference number: A34474; MUID:90008924; PMID:2477373  
A;Accession: A34474  
A;Molecule type: DNA  
A;Residues: 1-1020 <SHU>  
A;Cross-references: UNIPROT:P50993; GB:J05096; NID:G179164; PIDN:AAA51797.1; PID:G179165  
R;Shull, M.M.; Lingrel, J.B.  
Proc. Natl. Acad. Sci. U.S.A. 84, 4039-4043, 1987  
A;Title: Multiple genes encode the human Na<sup>+</sup>, K<sup>+</sup>-ATPase catalytic subunit.  
A;Reference number: A94158; MUID:87231946; PMID:3035563  
A;Accession: B27795  
A;Molecule type: DNA  
A;Residues: 211-249 <SH2>  
A;Cross-references: GB:M16795; NID:G179196; PIDN:AAA51799.1; PID:G553194  
R;Sverdlov, E.D.; Monastyrskaya, G.S.; Broude, N.E.; Ushkaryov, Y.A.; Allikmets, R.L.; M  
tina, M.B.; Sverdlov, V.E.; Modyanov, N.N.; Ovchinnikov, Y.A.  
FEBS Lett. 217, 275-278, 1987  
A;Title: The family of human Na<sup>+</sup>, K<sup>+</sup>-ATPase genes. No less than five genes and/or pseudog  
A;Reference number: A27397; MUID:87247232; PMID:3036582  
A;Accession: D27397  
A;Molecule type: DNA  
A;Residues: 251-442 <SVE>  
A;Cross-references: GB:M27571  
C;Genetics:  
A;Gene: GDB:ATPIA2  
A;Cross-references: GDB:119712; OMIM:182340  
A;Map position: 1q21-q23  
C;Superfamily: Na<sup>+</sup>/K<sup>+</sup>-transporting ATPase alpha chain; ATPase nucleotide-binding domain  
C;Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium trans;  
F;6-93/Domain: Na<sup>+</sup>/K<sup>+</sup>-transporting ATPase alpha-2 chain #status predicted <INT1>  
F;94-118/Domain: intracellular #status predicted <TM1>  
F;128-147/Domain: transmembrane #status predicted <TM2>  
F;148-288/Domain: intracellular #status predicted <INT2>  
F;289-311/Domain: transmembrane #status predicted <TM3>  
F;318-346/Domain: transmembrane #status predicted <TM4>  
F;347-783/Domain: intracellular #status predicted <INT3>

F:584-780/Domain: ATPase nucleotide-binding domain homology <ATN>  
 F:784-807/Domain: transmembrane #status predicted <TM5>  
 F:846-871/Domain: transmembrane #status predicted <TM6>  
 F:872-949/Domain: intracellular #status predicted <INT4>  
 F:950-975/Domain: transmembrane #status predicted <TM7>  
 F:976-1020/Domain: extracellular #status predicted <EXT>  
 F:374/Active site: Asp (aspartylphosphate intermediate) #status predicted  
 F:505/Binding site: ATP (lys) #status predicted  
 F:714,718,723/Active site: Asp, Asp, Lys #status predicted

Query Match 50.6%; Score 43; DB 2; Length 1020;  
 Best Local Similarity 60.0%; Pred. No. 65;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 5 PTLREWISFC 14  
 || ||: ||  
 Db 82 PTPPEWVKFC 91

RESULT 12  
 B24639  
 Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-2 chain - rat  
 N:Alternate names: Na+/K+-transporting ATPase alpha-plus chain  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 30-Jun-1988 #sequence\_revision 30-Jun-1988 #text\_change 09-Jul-2004  
 C:Accession: B24639  
 R:Shull, G.E.; Greeb, J.; Lingrel, J.B.  
 Biochemistry 25, 8125-8132, 1986  
 A:Title: Molecular cloning of three distinct forms of the Na+, K+-ATPase alpha-subunit from Rattus norvegicus  
 A:Reference number: A90512; PMID:87128908; PMID:3028470  
 A:Accession: B24639  
 A:Molecule type: mRNA  
 A:Residues: 1-1020 <SHU>  
 A:Cross-references: UNIPROT:P06686; EMBL:M14512; NID:g203028; PIDN:AAA40776.1; PID:g203028  
 C:Genetics:  
 A:Gene: NKAA2  
 C:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain  
 C:Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transport  
 F:6-1020/Product: Na+/K+-transporting ATPase alpha-2 chain #status predicted <MAT>  
 F:6-93/Domain: intracellular #status predicted <INT1>  
 F:94-119/Domain: transmembrane #status predicted <TM1>  
 F:128-147/Domain: transmembrane #status predicted <TM2>  
 F:148-288/Domain: intracellular #status predicted <INT2>  
 F:289-311/Domain: transmembrane #status predicted <TM3>  
 F:318-346/Domain: transmembrane #status predicted <TM4>  
 F:347-783/Domain: intracellular #status predicted <INT3>  
 F:584-780/Domain: ATPase nucleotide-binding domain homology <ATN>  
 F:784-807/Domain: transmembrane #status predicted <TM5>  
 F:846-871/Domain: transmembrane #status predicted <TM6>  
 F:872-949/Domain: intracellular #status predicted <INT4>  
 F:950-975/Domain: transmembrane #status predicted <TM7>  
 F:976-1020/Domain: extracellular #status predicted <EXT>  
 F:374/Active site: Asp (aspartylphosphate intermediate) #status predicted  
 F:505/Binding site: ATP (lys) #status predicted  
 F:714,718,723/Active site: Asp, Asp, Lys #status predicted

Query Match 50.6%; Score 43; DB 2; Length 1020;  
 Best Local Similarity 60.0%; Pred. No. 65;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 5 PTLREWISFC 14  
 || ||: ||  
 Db 82 PTPPEWVKFC 91

RESULT 13  
 PWSHNA  
 Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain precursor - sheep  
 N:Alternate names: sodium pump alpha chain; sodium/potassium-dependent ATPase alpha chain  
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
 C:Date: 17-Mar-1987 #sequence\_revision 17-Mar-1987 #text\_change 09-Jul-2004  
 C:Accession: A01074; A35426  
 R:Shull, G.E.; Schwartz, A.; Lingrel, J.B.

Nature 316, 691-695, 1985  
 A:Title: Amino-acid sequence of the catalytic subunit of the (Na(+)+K(+)) ATPase deduced from complementary DNA  
 A:Reference number: A01074; PMID:85296299; PMID:2993903  
 A:Accession: A01074  
 A:Molecule type: mRNA  
 A:Residues: 1-1021 <SHU>  
 A:Cross-references: UNIPROT:P04074; GB:X02813; NID:g1205; PIDN:CAA26581.1; PID:g1206  
 J:Hintz, H.R.; Kirtley, T.L.  
 J. Biol. Chem. 265, 10260-10265, 1990  
 A:Title: Lysozyme 480 is an essential residue in the putative ATP site of lamb kidney (Na, K)-ATPase  
 A:Reference number: A35426; PMID:90285144; PMID:2162343  
 A:Accession: A35426  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 475-492 <HIN>  
 C:Comment: This is the catalytic component of the active enzyme, which catalyzes the hydrolysis of ATP to ADP and inorganic phosphate, providing the energy for active transport of Na+ and K+ across the cell membrane.  
 C:Comment: This enzyme is specifically inhibited by cardiac glycosides such as digoxin and ouabain.  
 C:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain  
 C:Keywords: ATP; hydrolase; phosphoprotein; potassium transport; sodium transport; transport; transmembrane  
 F:6-1021/Product: Na+/K+-transporting ATPase alpha chain #status predicted <MAT>  
 F:94-115/Domain: transmembrane #status predicted <TM1>  
 F:128-144/Domain: transmembrane #status predicted <TM2>  
 F:289-311/Domain: transmembrane #status predicted <TM3>  
 F:318-346/Domain: transmembrane #status predicted <TM4>  
 F:347-781/Domain: ATPase nucleotide-binding domain homology <ATN>  
 F:585-781/Domain: transmembrane #status predicted <TM5>  
 F:785-808/Domain: transmembrane #status predicted <TM6>  
 F:847-972/Domain: transmembrane #status predicted <TM7>  
 F:951-976/Domain: transmembrane #status predicted <TM8>  
 F:315/Binding site: cardiac glycoside (Trp) #status predicted  
 F:374/Active site: Asp (aspartylphosphate intermediate) #status predicted  
 F:506/Binding site: ATP (Lys) #status predicted

Query Match 50.6%; Score 43; DB 1; Length 1021;  
 Best Local Similarity 60.0%; Pred. No. 65;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 5 PTLREWISFC 14  
 || ||: ||  
 Db 82 PTPPEWVKFC 91

RESULT 14  
 S04630  
 Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-1 chain - horse  
 C:Species: Equus caballus (domestic horse)  
 C:Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 09-Jul-2004  
 C:Accession: S04630  
 R:Kano, I.; Nagai, F.; Satoh, K.; Ushiyama, K.; Nakao, T.; Kano, K.  
 FEBS Lett. 250, 91-98, 1989  
 A:Title: Structure of the alpha(1) subunit of horse Na,K-ATPase gene.  
 A:Reference number: S04630; PMID:89290042; PMID:2544461  
 A:Accession: S04630  
 A:Molecule type: DNA  
 A:Residues: 1-1021 <KAN>  
 A:Cross-references: UNIPROT:P18907; EMBL:X16773; NID:g1010; PIDN:CAA34716.1; PID:g871026  
 C:Genetics:  
 A:Introns: 4/3; 39/3; 59/3; 127/3; 165/3; 210/3; 250/1; 339/3; 406/1; 442/3; 487/3; 552/3; 552/3  
 C:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain  
 C:Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transport  
 F:6-1021/Product: Na+/K+-transporting ATPase alpha-1 chain #status predicted <MAT>  
 F:6-93/Domain: intracellular #status predicted <INT1>  
 F:94-118/Domain: transmembrane #status predicted <TM1>  
 F:128-147/Domain: transmembrane #status predicted <TM2>  
 F:148-288/Domain: intracellular #status predicted <INT2>  
 F:289-311/Domain: transmembrane #status predicted <TM3>  
 F:318-346/Domain: transmembrane #status predicted <TM4>  
 F:347-784/Domain: intracellular #status predicted <INT3>  
 F:585-781/Domain: transmembrane #status predicted <TM5>  
 F:785-808/Domain: transmembrane #status predicted <TM6>  
 F:847-872/Domain: transmembrane #status predicted <TM7>  
 F:873-950/Domain: intracellular #status predicted <INT4>

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F:951-976/Domain: transmembrane #status predicted <TM7>
F:977-1021/Domain: extracellular #status predicted <EXT>
F:374/Active site: Asp (aspartylphosphate intermediate) #status predicted
F:506/Binding site: ATP (lys) #status predicted
F:715,719,724/Active site: Asp, Asp, Lys #status predicted

Query Match          50.6%; Score 43; DB 1; Length 1021;
Best Local Similarity 60.0%; Pred. No. 65;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PTLREWISFC 14
Db 82 PTPPEWVKFC 91

RESULT 15
A28199
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - chicken
C:Species: Gallus gallus (chicken)
C:Date: 21-Sep-1988 #sequence_revision 21-Sep-1988 #text_change 09-Jul-2004
C:Accession: A28199
R:Takeyasu, K.; Tamkun, M.M.; Renaud, K.J.; Fambrough, D.M.
J. Biol. Chem. 263 4347-4354, 1988
A:Title: Ouabain-sensitive (Na(+) + K(+))-ATPase activity expressed in mouse L cells by
A:Reference number: A28199; MUID:88153759; PMID:2831227
A:Accession: A28199
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1021 <TAK>
A:Cross-references: UNIPROT:P09572; GB:J03230; NID:g211219; PTDN:AAA48607.1; PID:g211220
C:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C:Keywords: ATP; glycoprotein; hydrolase; phosphoprotein; transmembrane protein
F:585-781/Domain: ATPase nucleotide-binding domain homology <ATN>
F:213,481/Binding site: carboxylate (Asn) (covalent) #status predicted
F:374/Active site: Asp (aspartylphosphate intermediate) #status predicted
F:506/Binding site: ATP (Lys) #status predicted

Query Match          50.6%; Score 43; DB 2; Length 1021;
Best Local Similarity 60.0%; Pred. No. 65;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PTLREWISFC 14
Db 82 PTPPEWVKFC 91

Search completed: January 31, 2005, 18:22:36
Job time : 30 secs

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